

# SSc

## BOPOHDR

11/13/2021

```
#Systemic Sclerosis statistics
##Legend
PNP = perifērā neiropātija
SNP = smalko šķiedru neiropātija
#Read data in
```

```
ssc <- read.table("SSc_PNP.txt", header=TRUE)
library(dplyr)
library(ggplot2)
library(magrittr)
library(stringr)
library(ggpubr)
library(cocor)
library(rmarkdown)
library(knitr)
```

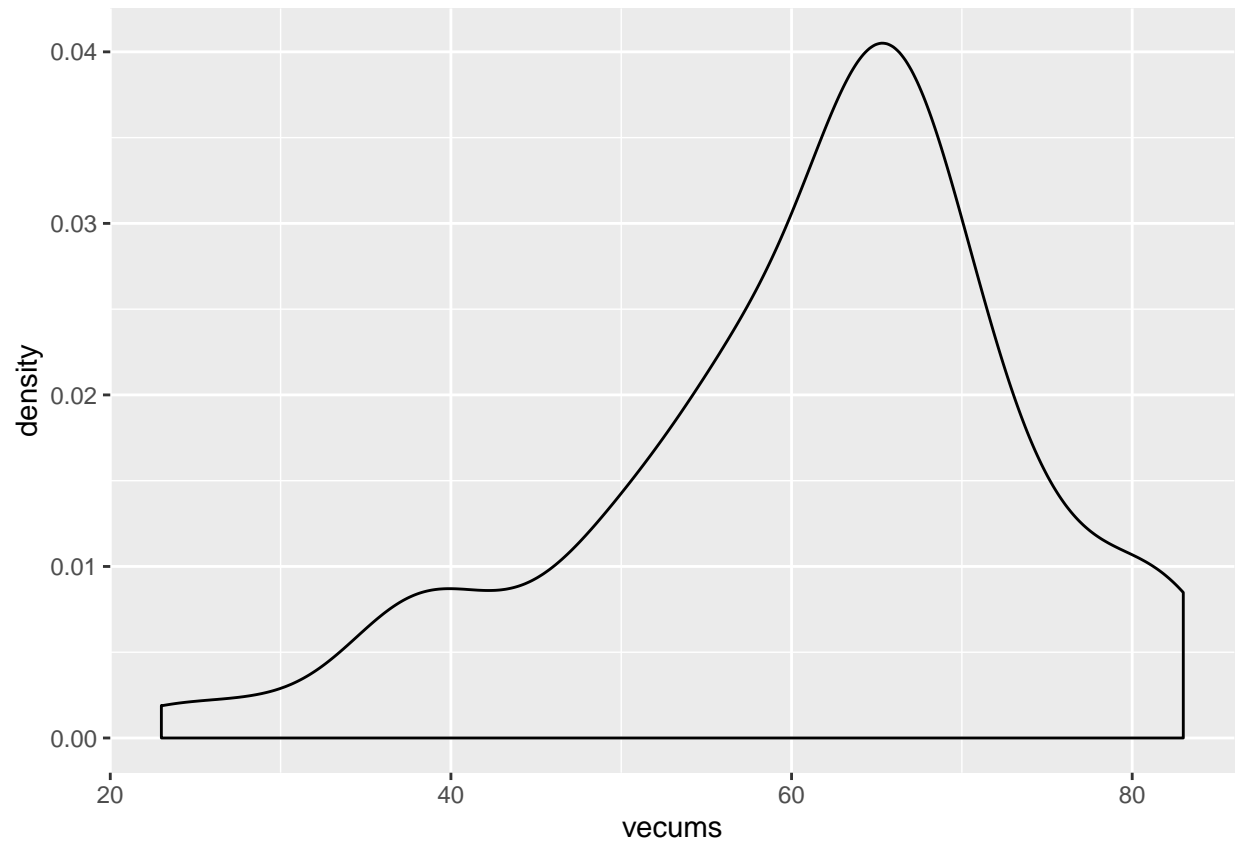
```
#Evaluate normality of the data
```

```
shp_vecums <- shapiro.test(ssc$vecums)
shp_total <- shapiro.test(ssc$Total)
shp_DN4 <- shapiro.test(ssc$DN4_total)
shp_GAD7 <- shapiro.test(ssc$GAD.7_total)
shp_HAQDI <- shapiro.test(ssc$HAQDI)
shp_Rodnan <- shapiro.test(ssc$Rodnan)
shp_ilgums <- shapiro.test(ssc$saslim_anas_ilgums_.gadi.)
rbind(shp_vecums,shp_total,shp_DN4,shp_GAD7,shp_HAQDI,shp_Rodnan,shp_ilgums)
```

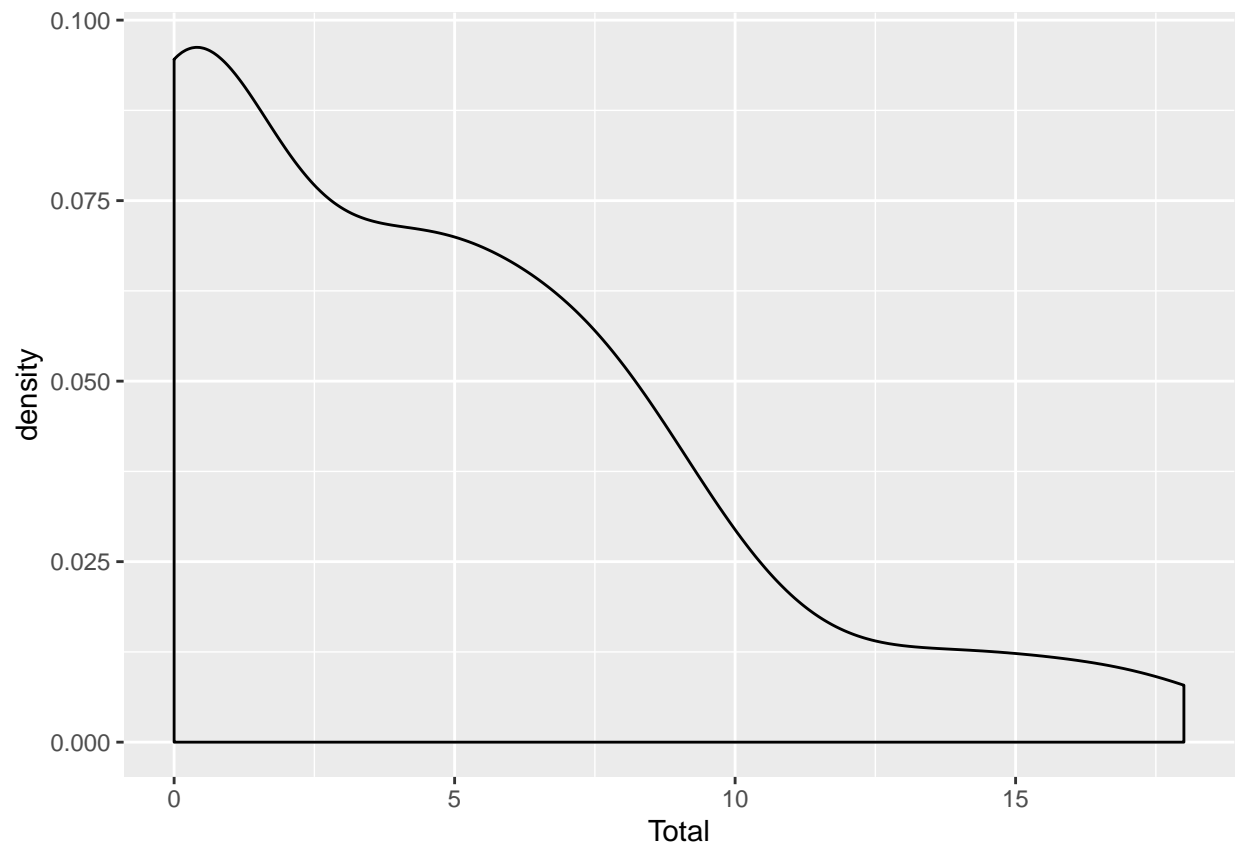
```
##          statistic p.value      method
## shp_vecums 0.9573956 0.01384063 "Shapiro-Wilk normality test"
## shp_total  0.8528337 5.358064e-07 "Shapiro-Wilk normality test"
## shp_DN4    0.838005  2.109071e-07 "Shapiro-Wilk normality test"
## shp_GAD7   0.862728  1.14325e-06  "Shapiro-Wilk normality test"
## shp_HAQDI  0.917084  0.0001431577 "Shapiro-Wilk normality test"
## shp_Rodnan 0.8122545 4.370257e-08 "Shapiro-Wilk normality test"
## shp_ilgums 0.871585  2.314777e-06 "Shapiro-Wilk normality test"
##          data.name
## shp_vecums "ssc$vecums"
## shp_total  "ssc$Total"
## shp_DN4    "ssc$DN4_total"
## shp_GAD7   "ssc$GAD.7_total"
```

```
## shp_HAQDI "ssc$HAQDI"  
## shp_Rodnan "ssc$Rodnan"  
## shp_ilgums "ssc$saslim_anas_ilgums_.gadi."
```

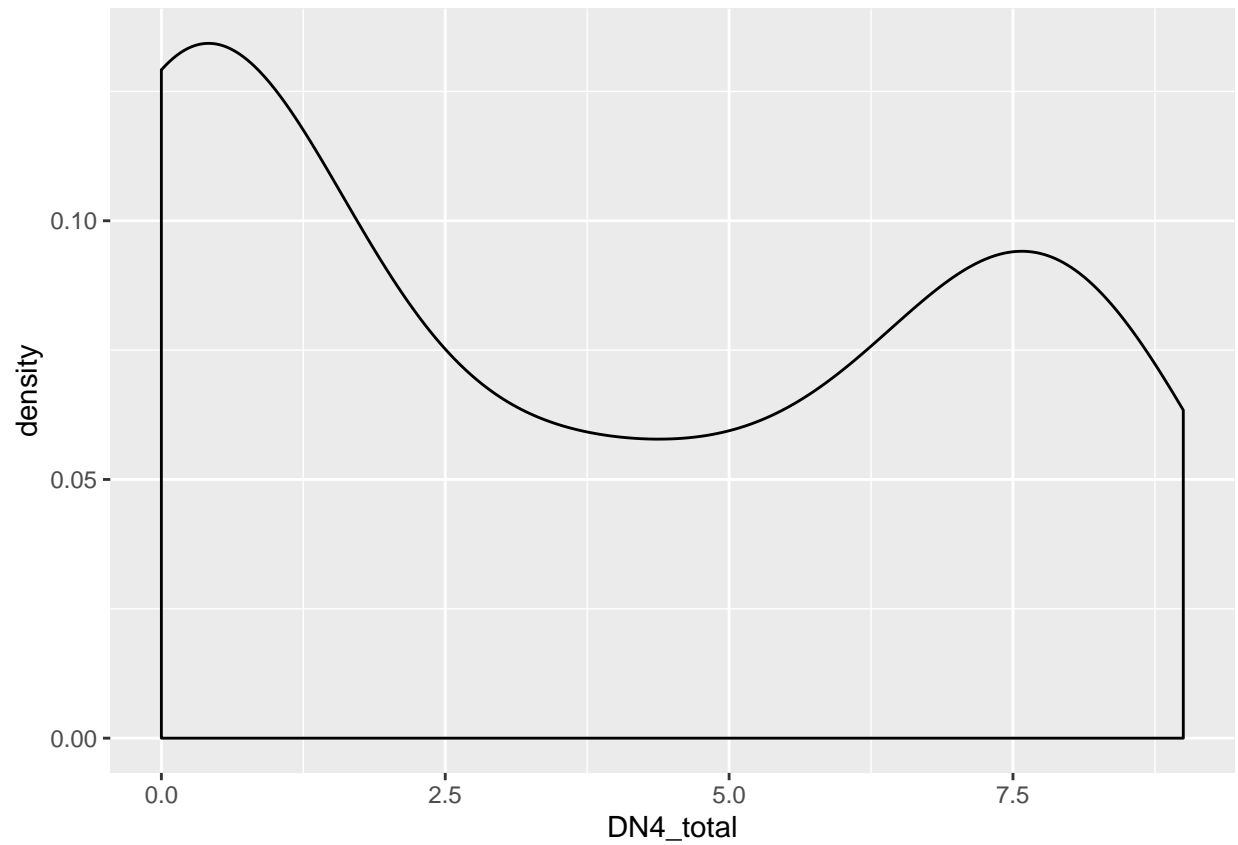
```
ssc %>% ggplot(aes(vecums))+geom_density()
```



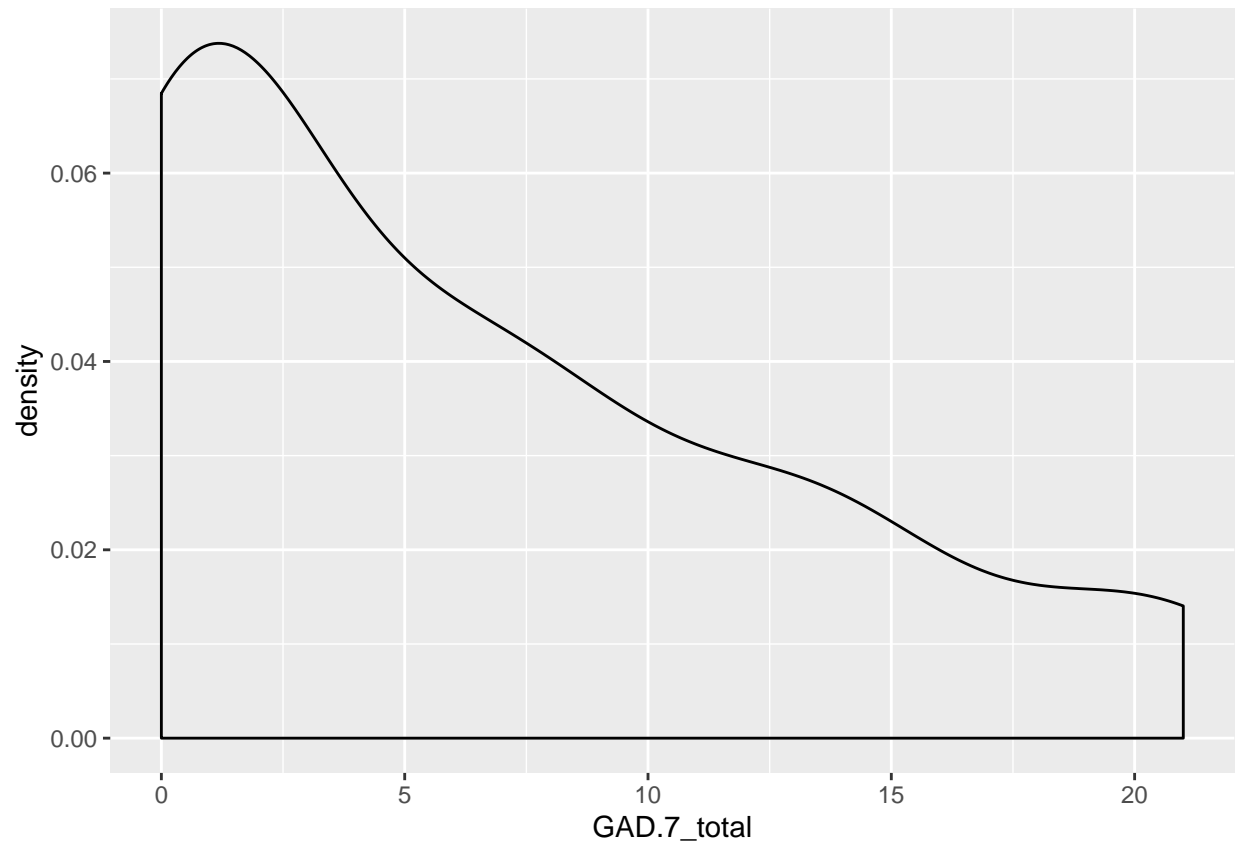
```
ssc %>% ggplot(aes(Total))+geom_density()
```



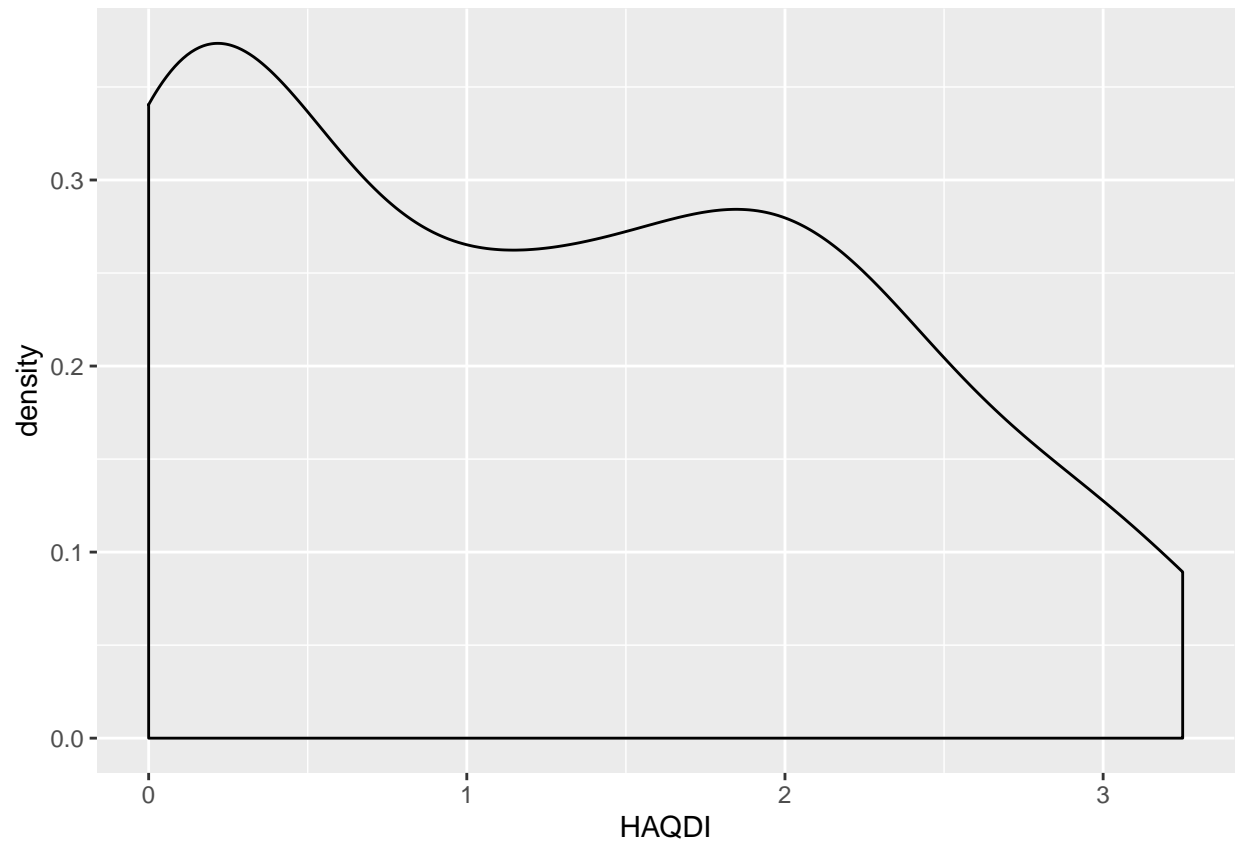
```
ssc %>% ggplot(aes(DN4_total))+geom_density()
```



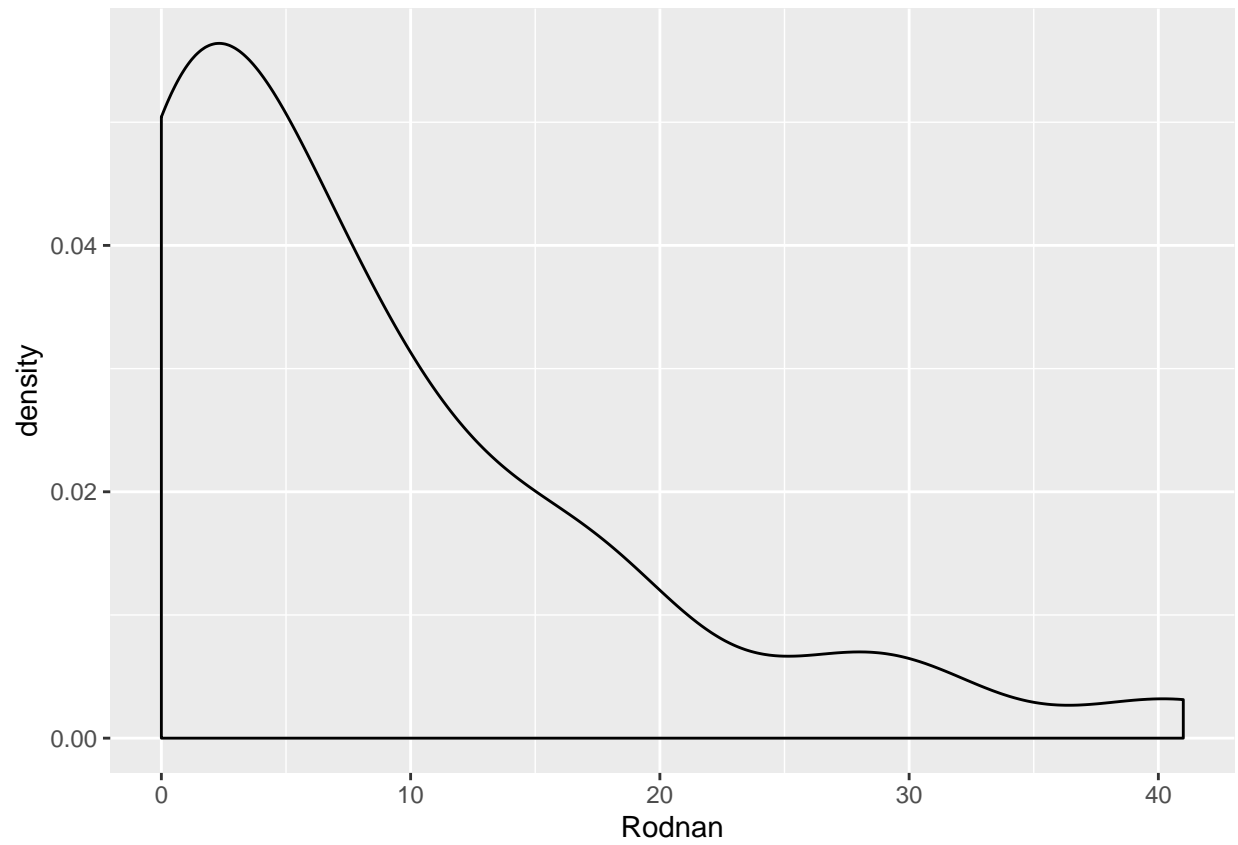
```
ssc %>% ggplot(aes(GAD.7_total))+geom_density()
```



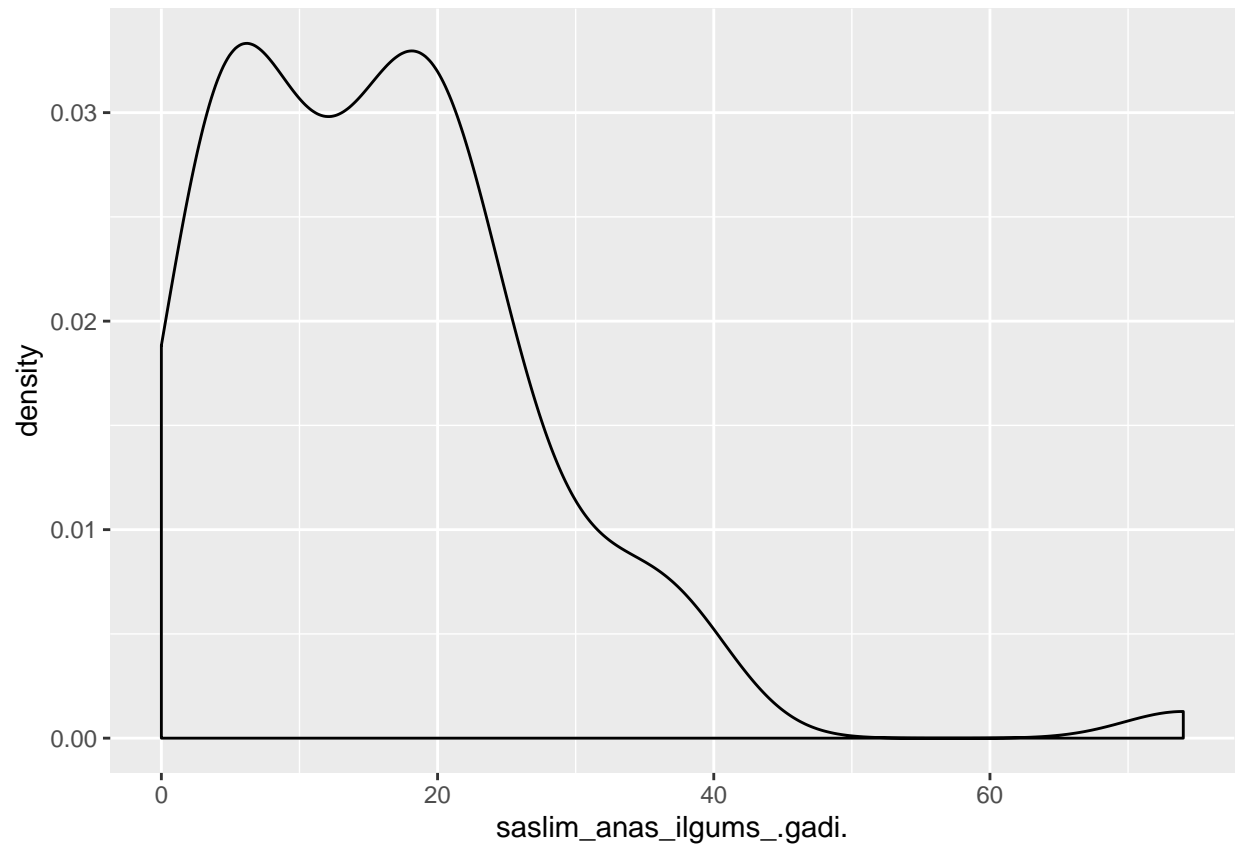
```
ssc %>% ggplot(aes(HAQDI))+geom_density()
```



```
ssc %>% ggplot(aes(Rodnan))+geom_density()
```



```
ssc %>% ggplot(aes(saslim_anas_ilgums_.gadi.))+geom_density()
```



In conclusion, all continuous data are not-normally distributed —

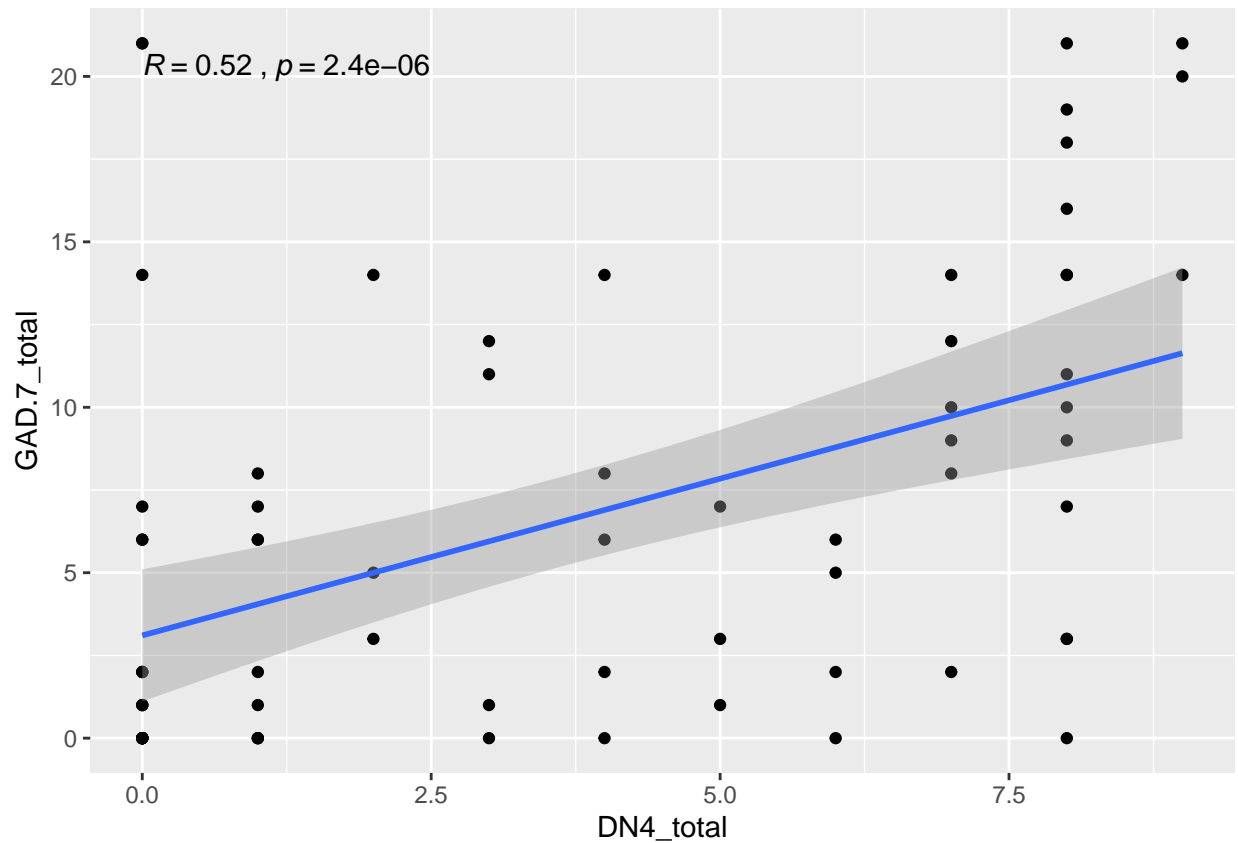
#Evaluate if GAD7 and DN4 corelate

```
cor(ssc$DN4_total,ssc$GAD.7_total,use='pairwise.complete.obs')
```

```
## [1] 0.4843338
```

```
ssc %>% ggplot(aes(DN4_total,GAD.7_total))+geom_point()+geom_smooth(method=lm)+stat_cor(method = "spearman")
```





In conclusion, DN4 and GAD7 have only moderate correlation, so will be evaluated separately

---

#Descriptives

##Vecums start PNP

```
pnp_vecums_tabula <- ssc %>% group_by(PNP_0.nav_1.ir) %>% summarize(
  count = table(PNP_0.nav_1.ir),
  mean = mean(vecums),
  SD = sd(vecums),
  median = median(vecums),
  IQR = IQR(vecums))
```

pnp\_vecums\_tabula

```
## # A tibble: 2 x 6
##   PNP_0.nav_1.ir count    mean    SD median    IQR
##         <int> <table> <dbl> <dbl> <int> <dbl>
## 1             0  31    53.8  12.9     56    21
## 2             1  43    66.1   9.97     66     8.5
```

##Vecums starp SNP

```
snp_vecums_tabula <- ssc %>% group_by(smalku___iedru_NP_0.nav_1.ir) %>% summarize(
  count = table(smalku___iedru_NP_0.nav_1.ir),
  mean = mean(vecums),
  SD = sd(vecums),
  median = median(vecums),
  IQR = IQR(vecums))
```

```
snp_vecums_tabula
```

```
## # A tibble: 2 x 6
##   smalku___iedru_NP_0.nav_1.ir count    mean    SD median    IQR
##             <int> <table> <dbl> <dbl> <int> <dbl>
## 1             0 45      64.4  12.1    66    10
## 2             1 29      55.5  12.1    57    16
```

##Dzimuma sadalījums PNP un SNP

```
dzimumatabula_pnp<-table(ssc$PNP_0.nav_1.ir,ssc$dzimums_0.v_rietiis_1.sieviete,dnn=c("dzimums_0.v_rietiis_1.sieviete","dzimums_0.v_rietiis_1.sieviete"))
dzimumatabula_snp <- table(ssc$smalku___iedru_NP_0.nav_1.ir,ssc$dzimums_0.v_rietiis_1.sieviete,dnn=c("dzimums_0.v_rietiis_1.sieviete","dzimums_0.v_rietiis_1.sieviete"))

dzimumatabula_pnp_snp <- rbind(dzimumatabula_pnp,dzimumatabula_snp)
colnames(dzimumatabula_pnp_snp)<-c("male","female")
rownames(dzimumatabula_pnp_snp)<-c("pnp nav","pnp ir","snp nav","snp ir")
dzimumatabula_pnp_snp
```

```
##           male female
## pnp nav     5      26
## pnp ir      8      35
## snp nav     8      37
## snp ir      5      24
```

##PNP/SNP risks ## Dzimuma saistība ar PNP un SNP prevalenci

```
chi_pnp <- chisq.test(dzimumatabula_pnp)
chi_snp <- chisq.test(dzimumatabula_snp)
chi_pnp_snp <- rbind(chi_pnp,chi_snp)
chi_pnp_snp[,c(3,4,5)]
```

```
##           p.value method
## chi_pnp 1      "Pearson's Chi-squared test with Yates' continuity correction"
## chi_snp 1      "Pearson's Chi-squared test with Yates' continuity correction"
##           data.name
## chi_pnp "dzimumatabula_pnp"
## chi_snp "dzimumatabula_snp"
```

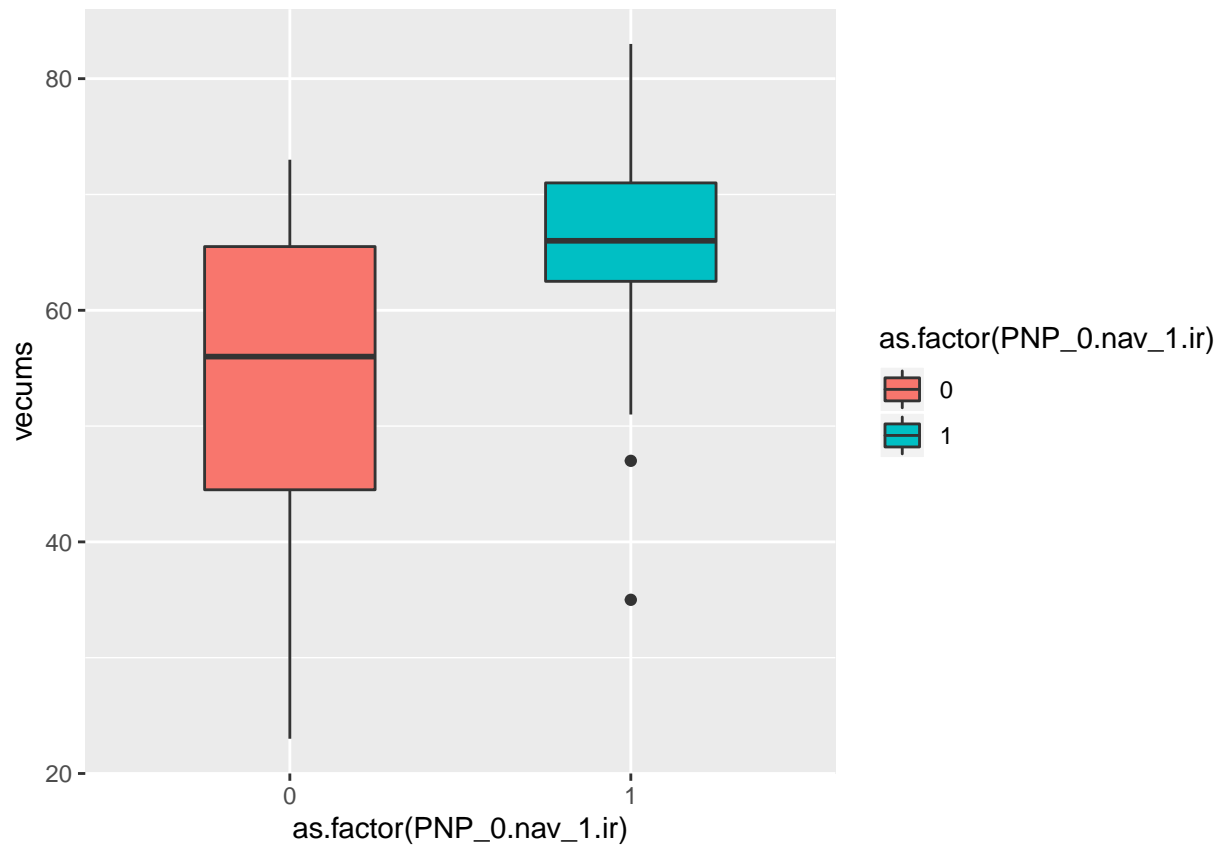
In conclusion, dzimums nav saistīts ar PNP vai SNP

##PNP risks ar vecumu ilgumu

```
kruskal.test(ssc$PNP_0.nav_1.ir~as.numeric(ssc$vecums))
```

```
##
## Kruskal-Wallis rank sum test
##
## data: ssc$PNP_0.nav_1.ir by as.numeric(ssc$vecums)
## Kruskal-Wallis chi-squared = 37.106, df = 36, p-value = 0.4178
```

```
ssc %>% ggplot(aes(as.factor(PNP_0.nav_1.ir),vecums,fill=as.factor(PNP_0.nav_1.ir)))+geom_boxplot(width=0.8)
```



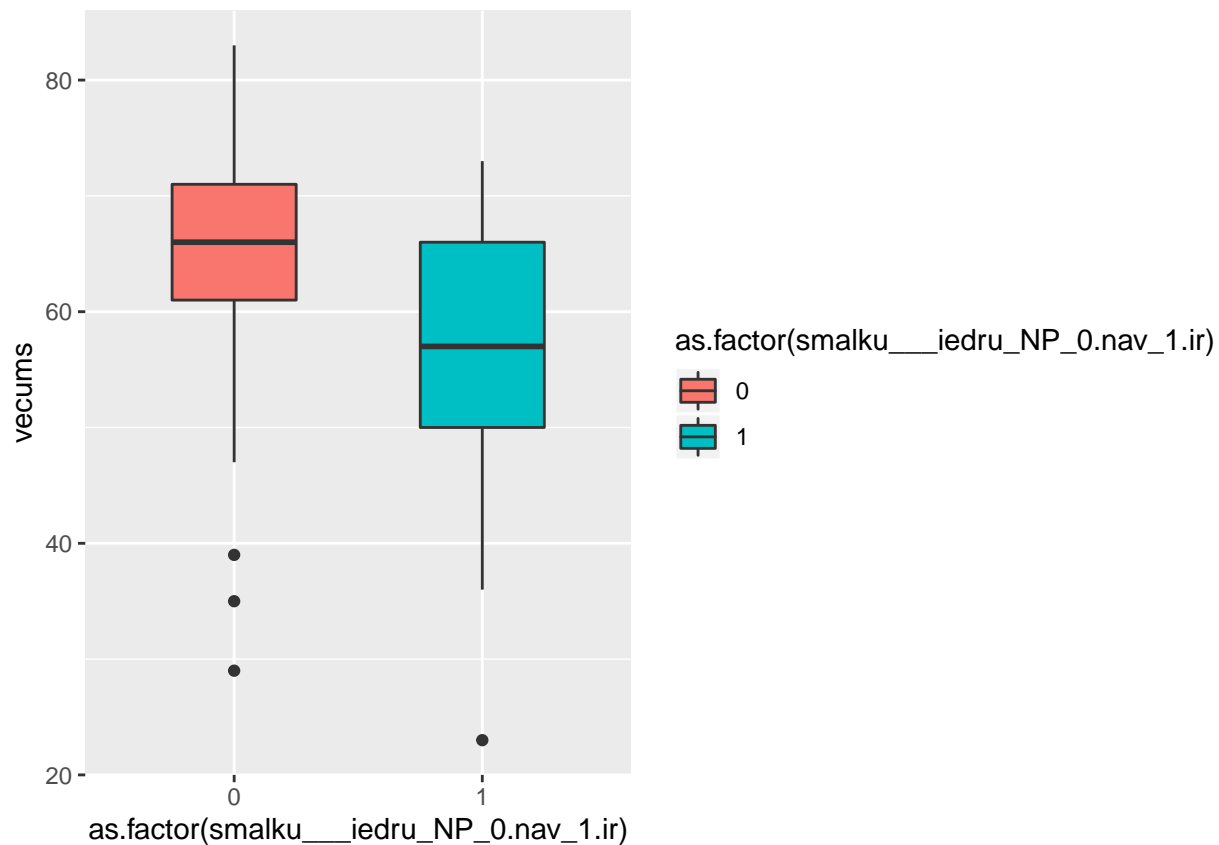
In conclusion, Pacienti ar PNP ir nedaudz vecāki (skat augstāk tabulu), bet starpība nav statistiski ticama

##SNP risks ar vecumu ilgumu

```
kruskal.test(ssc$smalku__iedru_NP_0.nav_1.ir~as.numeric(ssc$vecums))
```

```
##
## Kruskal-Wallis rank sum test
##
## data: ssc$smalku__iedru_NP_0.nav_1.ir by as.numeric(ssc$vecums)
## Kruskal-Wallis chi-squared = 33.232, df = 36, p-value = 0.601
```

```
ssc %>% ggplot(aes(as.factor(smalku__iedru_NP_0.nav_1.ir),vecums,fill=as.factor(smalku__iedru_NP_0.nav_1.ir)))+geom_boxplot(width=0.8)
```



In conclusion, Pacienti ar SNP ir nedaudz jaunāki (skat augstāk tabulu), bet starpība nav statistiski ticama

## PNP risks ar vecumu ilgumu

```
kruskal.test(ssc$PNP_0.nav_1.ir~as.numeric(ssc$saslim_anas_ilgums_.gadi.))
```

```
##
```

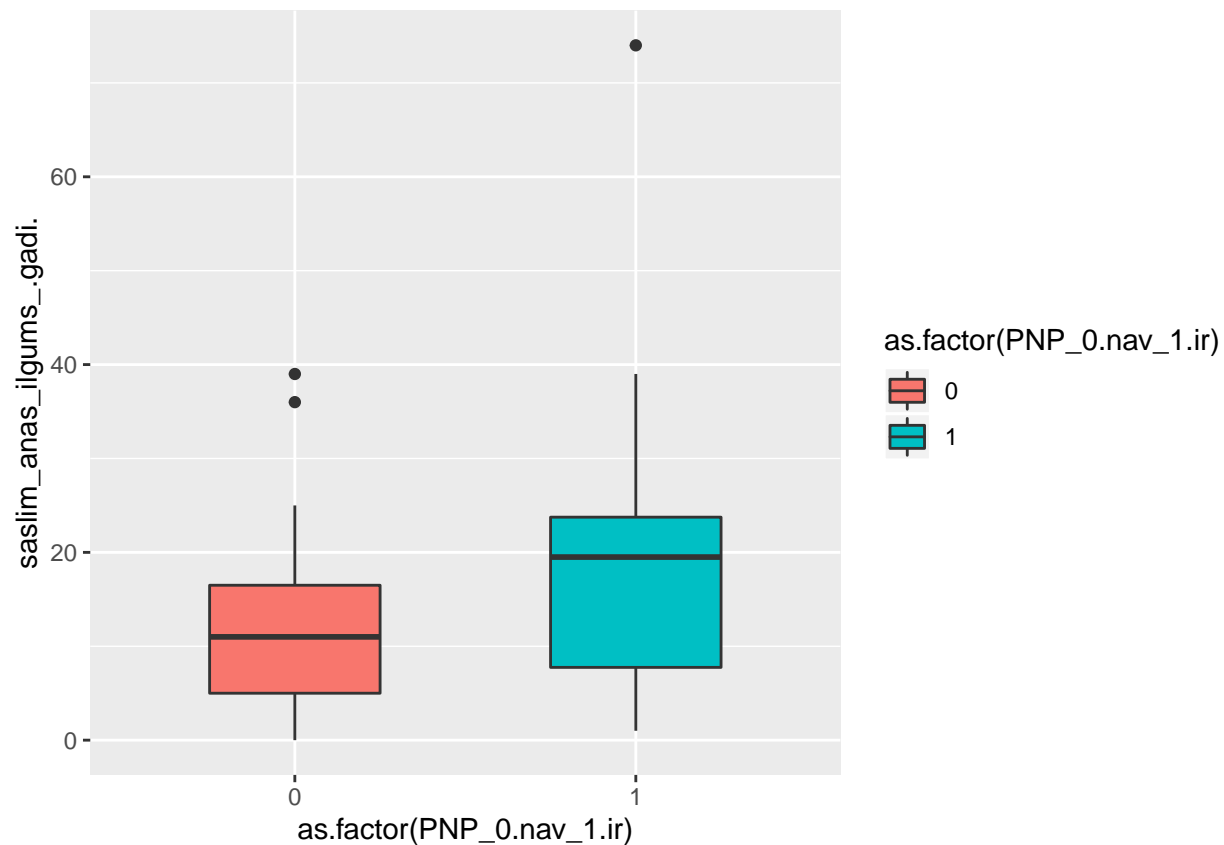
```
## Kruskal-Wallis rank sum test
```

```
##
```

```
## data: ssc$PNP_0.nav_1.ir by as.numeric(ssc$saslim_anas_ilgums_.gadi.)
```

```
## Kruskal-Wallis chi-squared = 25.509, df = 30, p-value = 0.7
```

```
ssc %>% ggplot(aes(as.factor(PNP_0.nav_1.ir),saslim_anas_ilgums_.gadi.,fill=as.factor(PNP_0.nav_1.ir)))
```

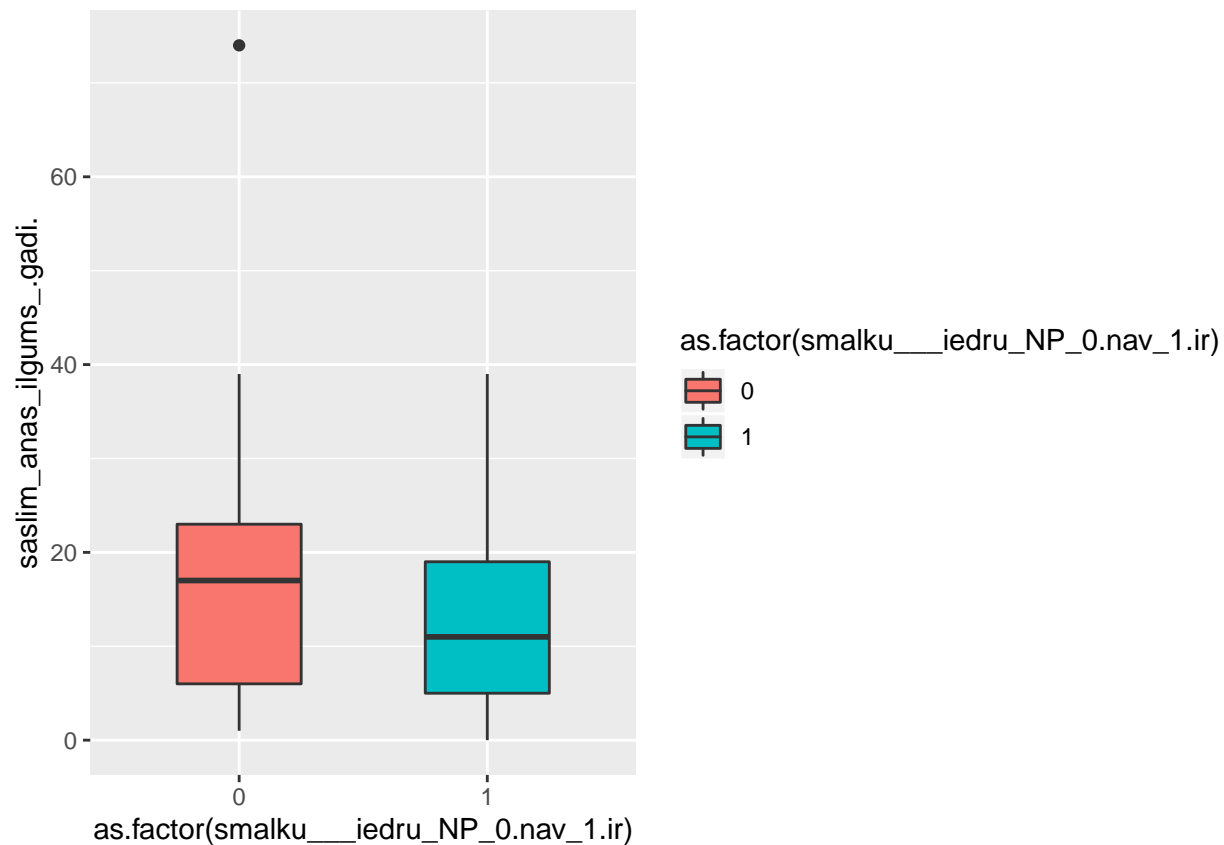


##SNP risks ar vecumu ilgumu

```
kruskal.test(ssc$smalku__iedru_NP_0.nav_1.ir~as.numeric(ssc$saslim_anas_ilgums_.gadi.))
```

```
##
## Kruskal-Wallis rank sum test
##
## data: ssc$smalku__iedru_NP_0.nav_1.ir by as.numeric(ssc$saslim_anas_ilgums_.gadi.)
## Kruskal-Wallis chi-squared = 22.227, df = 30, p-value = 0.8456
```

```
ssc %>% ggplot(aes(as.factor(smalku__iedru_NP_0.nav_1.ir),saslim_anas_ilgums_.gadi.,fill=as.factor(sma
```



In conclusion, PNP un SNP nav saistīti ar saslimšanas ilgumu

## PNP risks ar vecumu ilgumu

```
kruskal.test(ssc$PNP_0.nav_1.ir~as.numeric(ssc$Rodnan))
```

```
##
```

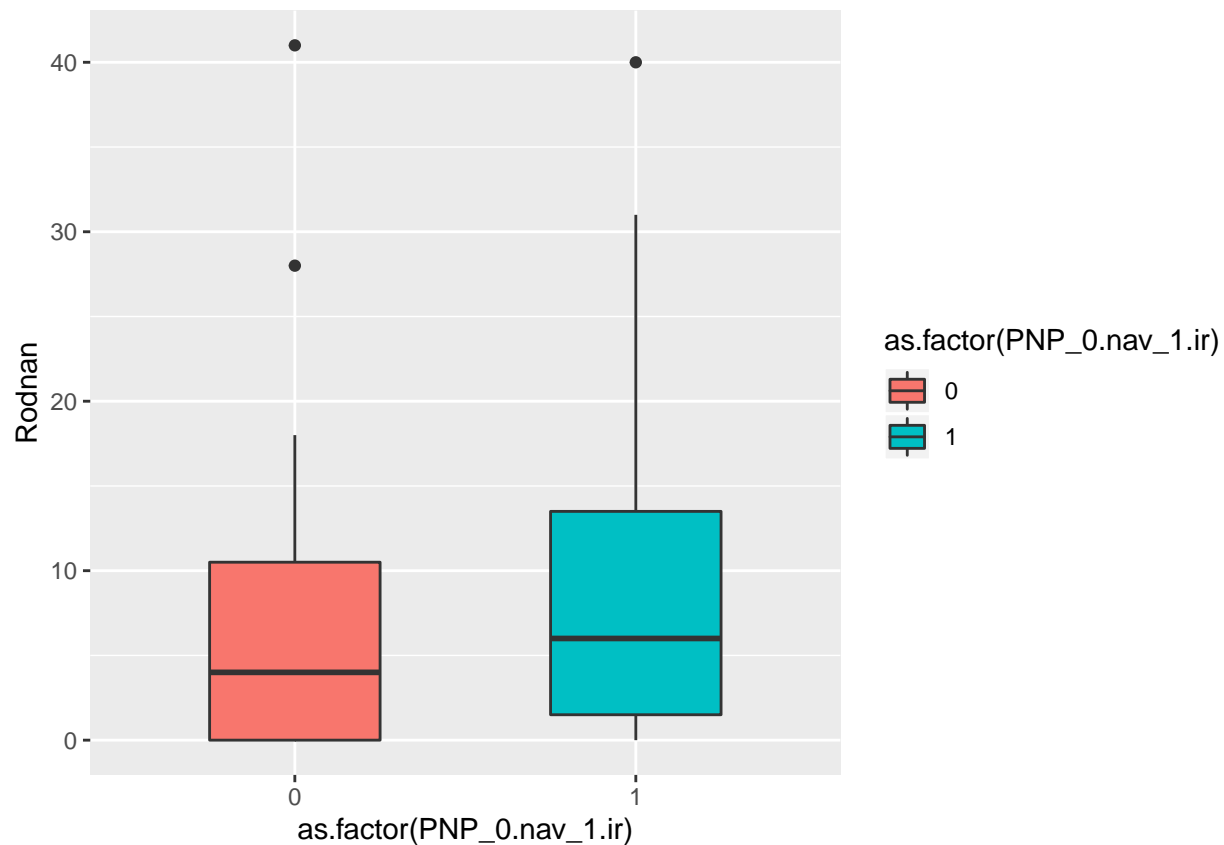
```
## Kruskal-Wallis rank sum test
```

```
##
```

```
## data: ssc$PNP_0.nav_1.ir by as.numeric(ssc$Rodnan)
```

```
## Kruskal-Wallis chi-squared = 19.918, df = 20, p-value = 0.4631
```

```
ssc %>% ggplot(aes(as.factor(PNP_0.nav_1.ir),Rodnan,fill=as.factor(PNP_0.nav_1.ir)))+geom_boxplot(width=0.5)
```

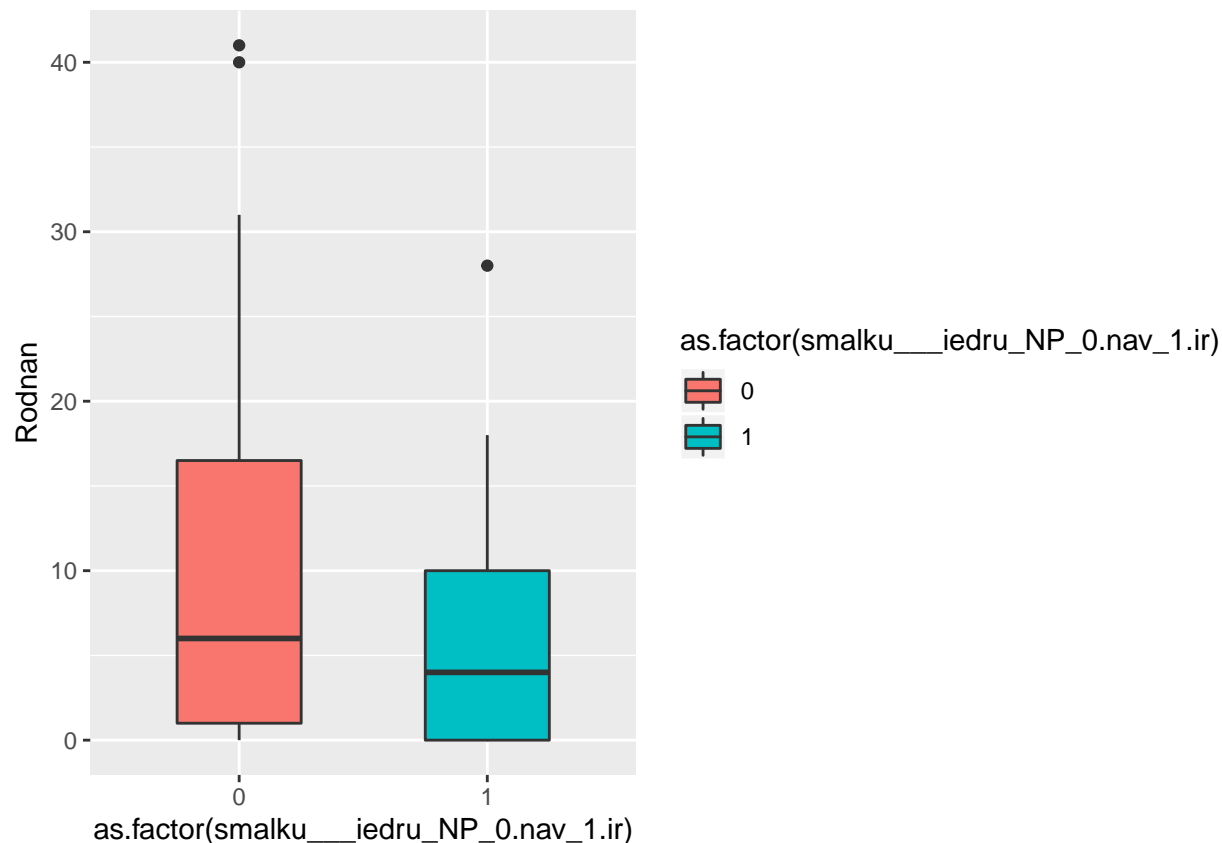


##SNP risks ar vecumu ilgumu

```
kruskal.test(ssc$smalku__iedru_NP_0.nav_1.ir~as.numeric(ssc$Rodnan))
```

```
##
## Kruskal-Wallis rank sum test
##
## data:  ssc$smalku__iedru_NP_0.nav_1.ir by as.numeric(ssc$Rodnan)
## Kruskal-Wallis chi-squared = 20.072, df = 20, p-value = 0.4534
```

```
ssc %>% ggplot(aes(as.factor(smalku__iedru_NP_0.nav_1.ir),Rodnan,fill=as.factor(smalku__iedru_NP_0.nav_1.ir)))
```



In conclusion, PNP un SNP nav saistīti ar slimības smagumu pēc Rodnan

##PNP un SNP saistība ar Reino

```
Reino_pnp<-table(ssc$PNP_0.nav_1.ir,ssc$Reino_sindroms_0.nav_1.ir,dnn=c("Reino_sindroms_0.nav_1.ir","PNP_0.nav_1.ir"))
Reino_snp <- table(ssc$smalku__iedru_NP_0.nav_1.ir,ssc$Reino_sindroms_0.nav_1.ir,dnn=c("Reino_sindroms_0.nav_1.ir","SNP_0.nav_1.ir"))
```

```
Reino_pnp_snp <- rbind(Reino_pnp,Reino_snp)
colnames(Reino_pnp_snp)<-c("Nav","Reino")
rownames(Reino_pnp_snp)<-c("pnp nav","pnp ir","snp nav","snp ir")
Reino_pnp_snp
```

```
##      Nav Reino
## pnp nav    5   26
## pnp ir     2   40
## snp nav     3   41
## snp ir      4   25
```

```
chi_pnp_Reino <- fisher.test(Reino_pnp)
chi_snp_Reino <- fisher.test(Reino_snp)
chi_pnp_snp_Reino <- rbind(chi_pnp_Reino,chi_snp_Reino)
chi_pnp_snp_Reino[,c(1,5,6,7)]
```

```
##      p.value alternative method
## chi_pnp_Reino 0.1269373 "two.sided" "Fisher's Exact Test for Count Data"
## chi_snp_Reino 0.4249522 "two.sided" "Fisher's Exact Test for Count Data"
```



```
## data.name
## chi_pnp_Reino "Reino_pnp"
## chi_snp_Reino "Reino_snp"
```

In conclusion, Reino fenomens nav saistīts ar PNP/SNP esamību

---

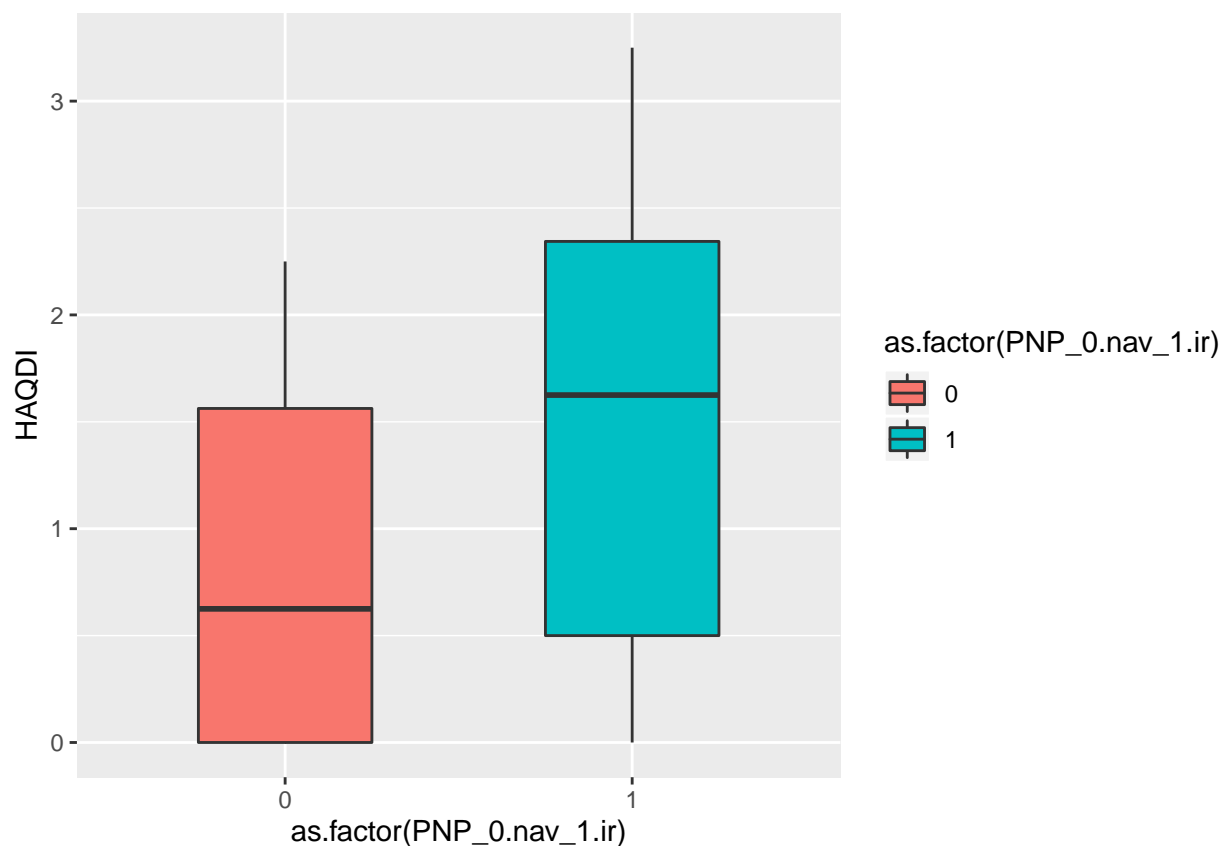
#PNP/SNP saistīb ar HAQDI, DN4 un GAD7

## PNP saistība ar HAQDI

```
kruskal.test(ssc$PNP_0.nav_1.ir~as.numeric(ssc$HAQDI))
```

```
##
## Kruskal-Wallis rank sum test
##
## data: ssc$PNP_0.nav_1.ir by as.numeric(ssc$HAQDI)
## Kruskal-Wallis chi-squared = 25.24, df = 25, p-value = 0.449
```

```
ssc %>% ggplot(aes(as.factor(PNP_0.nav_1.ir),HAQDI,fill=as.factor(PNP_0.nav_1.ir)))+geom_boxplot(width=
```

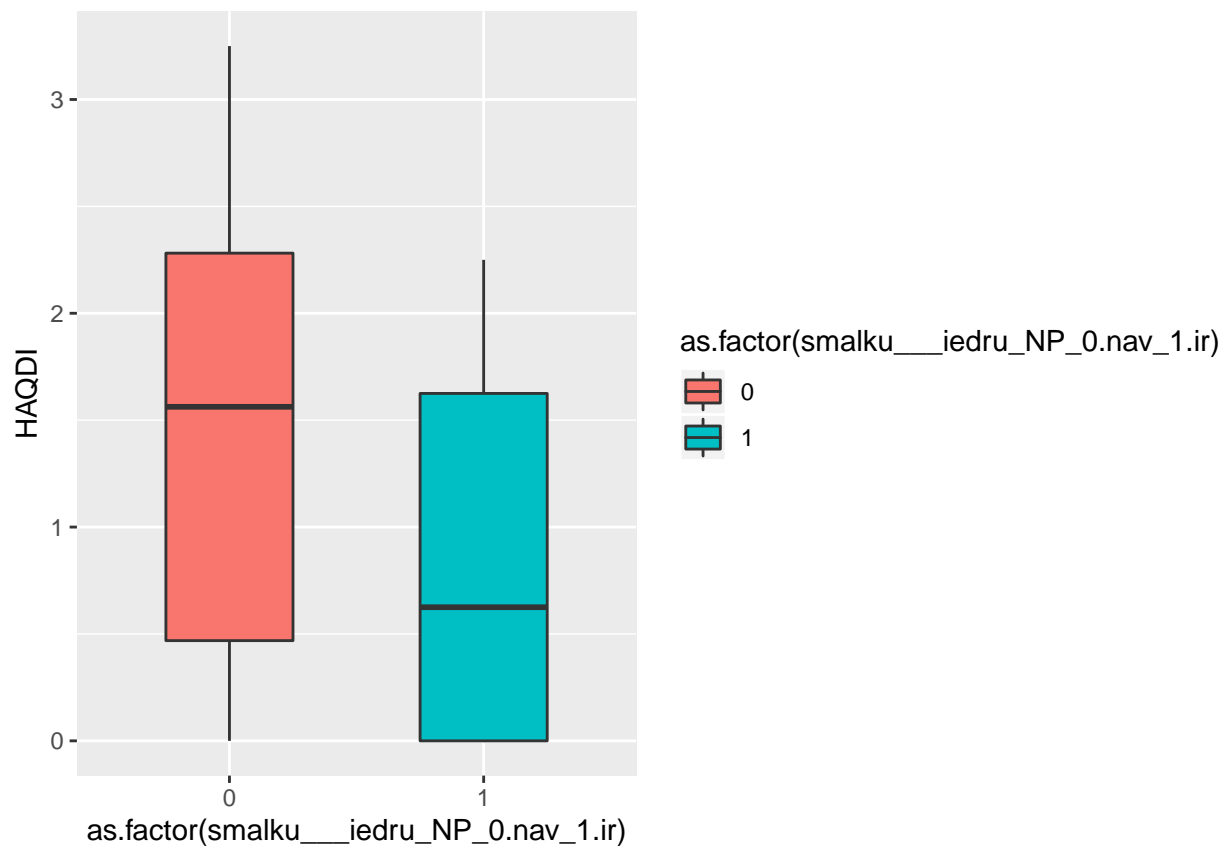


## SNP saistība ar HAQDI

```
kruskal.test(ssc$smalku___iedru_NP_0.nav_1.ir~as.numeric(ssc$HAQDI))
```

```
##  
## Kruskal-Wallis rank sum test  
##  
## data: ssc$smalku___iedru_NP_0.nav_1.ir by as.numeric(ssc$HAQDI)  
## Kruskal-Wallis chi-squared = 20.58, df = 25, p-value = 0.7158
```

```
ssc %>% ggplot(aes(as.factor(smalku___iedru_NP_0.nav_1.ir),HAQDI,fill=as.factor(smalku___iedru_NP_0.nav_1.ir))
```



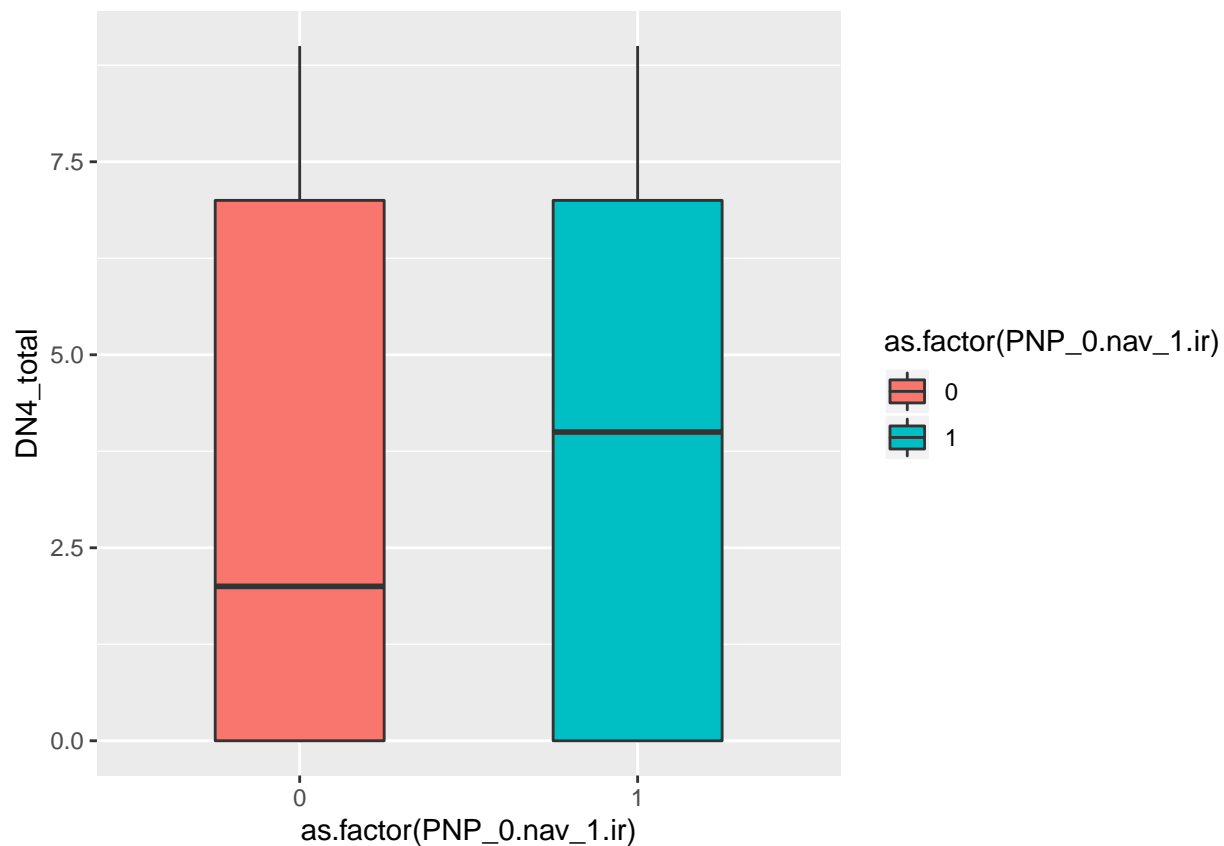
HAQDI neatšķirās starp pacientiem ar PNP/SNP un bez

## PNP saistība ar DN4

```
kruskal.test(ssc$PNP_0.nav_1.ir~as.numeric(ssc$DN4_total))
```

```
##  
## Kruskal-Wallis rank sum test  
##  
## data: ssc$PNP_0.nav_1.ir by as.numeric(ssc$DN4_total)  
## Kruskal-Wallis chi-squared = 5.1986, df = 9, p-value = 0.8167
```

```
ssc %>% ggplot(aes(as.factor(PNP_0.nav_1.ir),DN4_total,fill=as.factor(PNP_0.nav_1.ir)))+geom_boxplot(wi
```

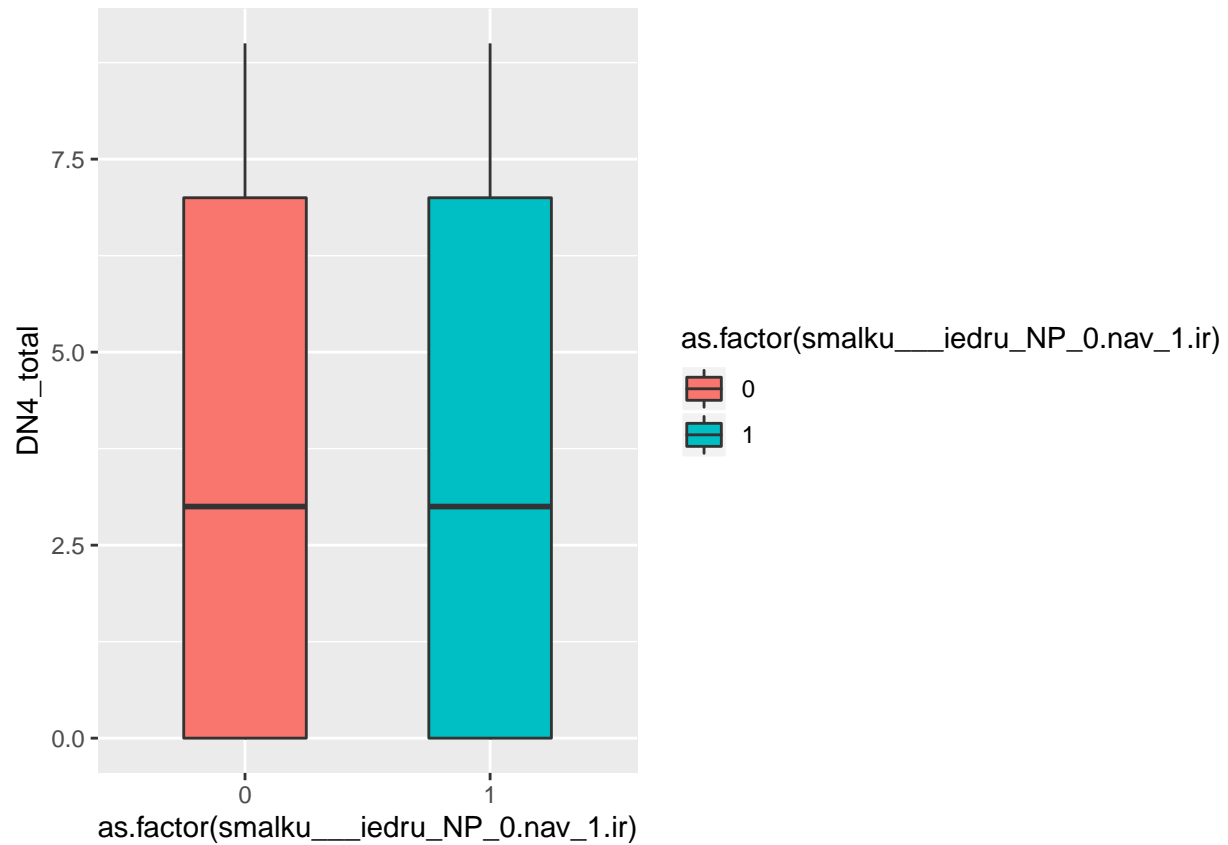


## SNP saistība ar DN4

```
kruskal.test(ssc$smalku__iedru_NP_0.nav_1.ir~as.numeric(ssc$DN4_total))
```

```
##
## Kruskal-Wallis rank sum test
##
## data: ssc$smalku__iedru_NP_0.nav_1.ir by as.numeric(ssc$DN4_total)
## Kruskal-Wallis chi-squared = 4.9156, df = 9, p-value = 0.8416
```

```
ssc %>% ggplot(aes(as.factor(smalku__iedru_NP_0.nav_1.ir),DN4_total,fill=as.factor(smalku__iedru_NP_0
```

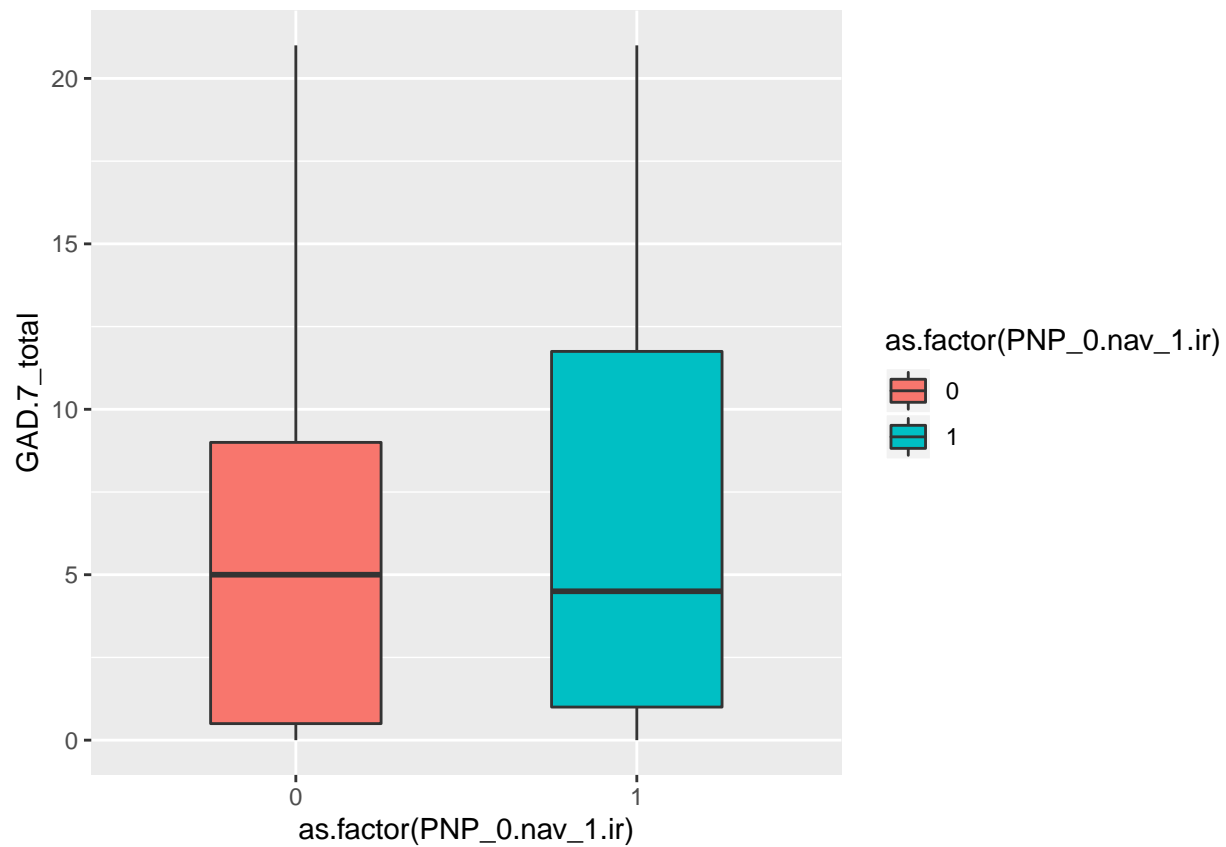


## PNP saistība ar GAD7

```
kruskal.test(ssc$PNP_0.nav_1.ir~as.numeric(ssc$GAD.7_total))
```

```
##
## Kruskal-Wallis rank sum test
##
## data: ssc$PNP_0.nav_1.ir by as.numeric(ssc$GAD.7_total)
## Kruskal-Wallis chi-squared = 16.333, df = 17, p-value = 0.5004
```

```
ssc %>% ggplot(aes(as.factor(PNP_0.nav_1.ir),GAD.7_total
,fill=as.factor(PNP_0.nav_1.ir)))+geom_boxplot(width=0.5)
```

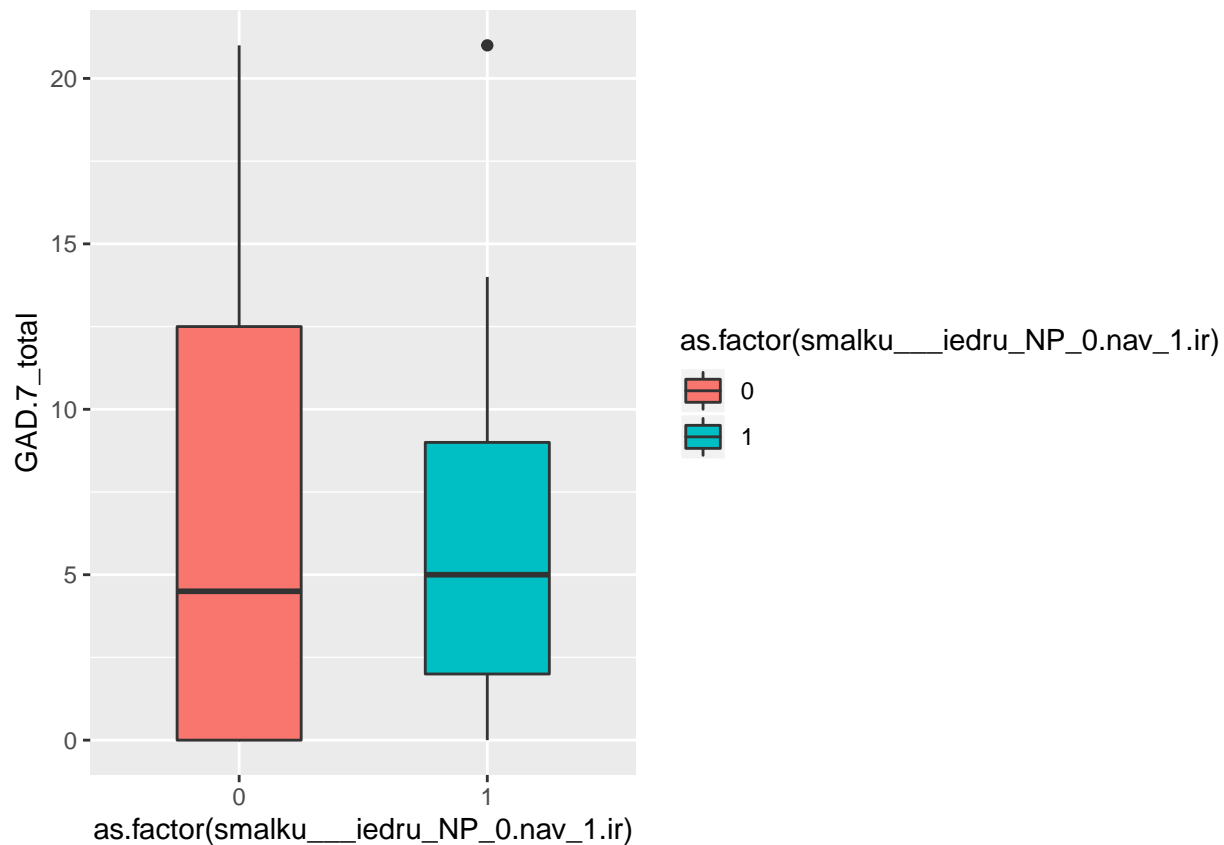


## SNP saistība ar GAD7

```
kruskal.test(ssc$smalku__iedru_NP_0.nav_1.ir~as.numeric(ssc$GAD.7_total))
```

```
##
## Kruskal-Wallis rank sum test
##
## data: ssc$smalku__iedru_NP_0.nav_1.ir by as.numeric(ssc$GAD.7_total)
## Kruskal-Wallis chi-squared = 17.601, df = 17, p-value = 0.4144
```

```
ssc %>% ggplot(aes(as.factor(smalku__iedru_NP_0.nav_1.ir),GAD.7_total,fill=as.factor(smalku__iedru_NP_0.nav_1.ir)))
```



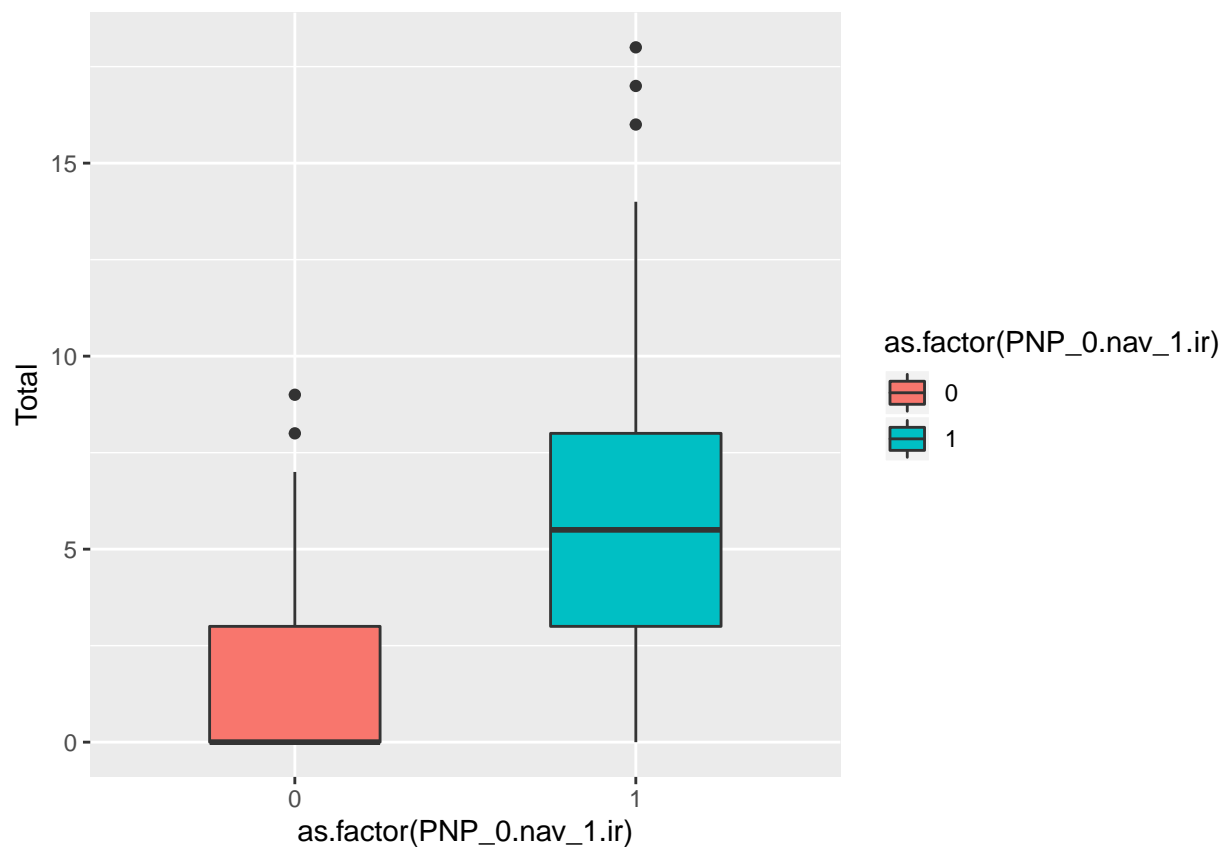
DN4 un GAD7 neatšķirās starp pacientiem ar PNP/SNP un bez

## PNP saistība ar Total TNS

```
kruskal.test(ssc$PNP_0.nav_1.ir~as.numeric(ssc$Total))
```

```
##
## Kruskal-Wallis rank sum test
##
## data: ssc$PNP_0.nav_1.ir by as.numeric(ssc$Total)
## Kruskal-Wallis chi-squared = 22.404, df = 15, p-value = 0.09763
```

```
ssc %>% ggplot(aes(as.factor(PNP_0.nav_1.ir),Total,fill=as.factor(PNP_0.nav_1.ir)))+geom_boxplot(width=
```

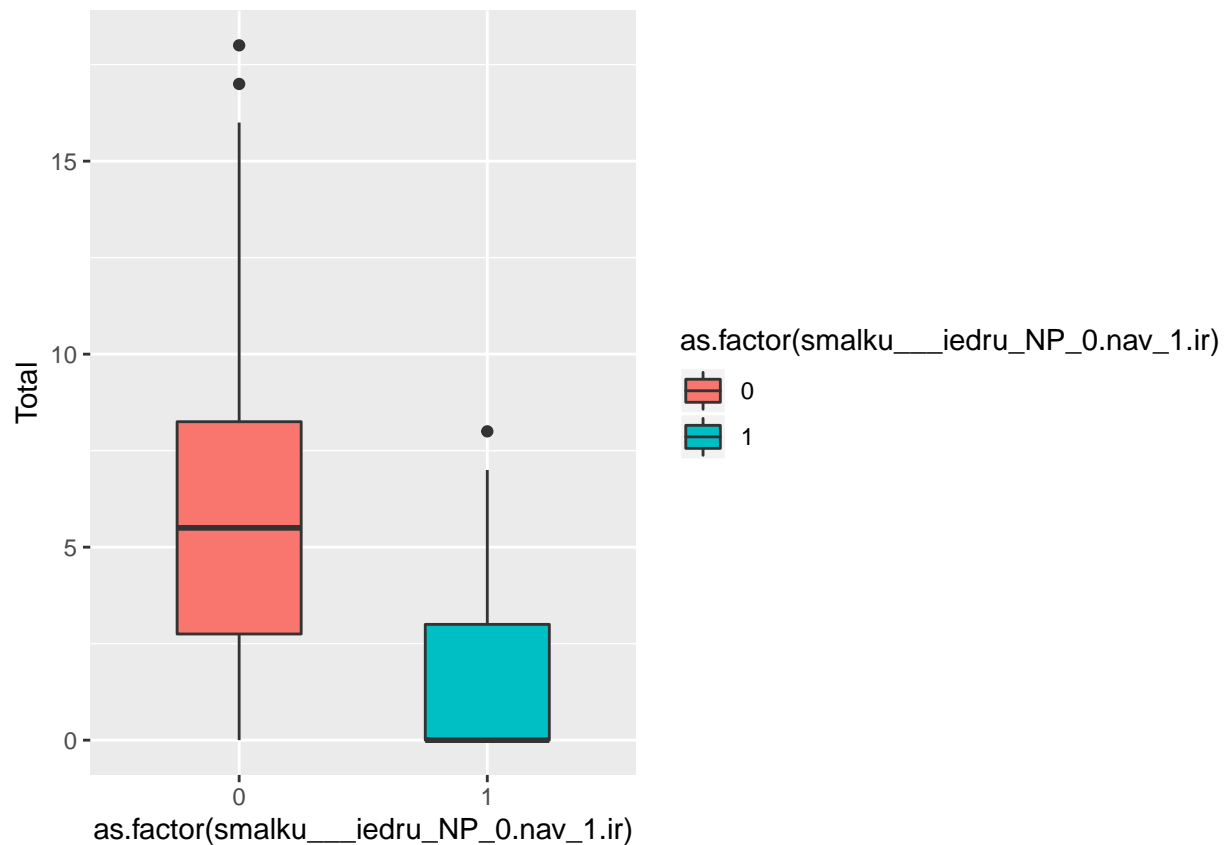


## SNP saistība ar HAQDI

```
kruskal.test(ssc$smalku__iedru_NP_0.nav_1.ir~as.numeric(ssc$Total))
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  ssc$smalku__iedru_NP_0.nav_1.ir by as.numeric(ssc$Total)
## Kruskal-Wallis chi-squared = 18.966, df = 15, p-value = 0.2153
```

```
ssc %>% ggplot(aes(as.factor(smalku__iedru_NP_0.nav_1.ir),Total,fill=as.factor(smalku__iedru_NP_0.nav_1.ir)))
```



Nav ticamas starpības starp TMS un PNP/SNP esamību??? kā?

---

```
#Total TNS saistība ar HAQDI, DN4 un GAD7
```

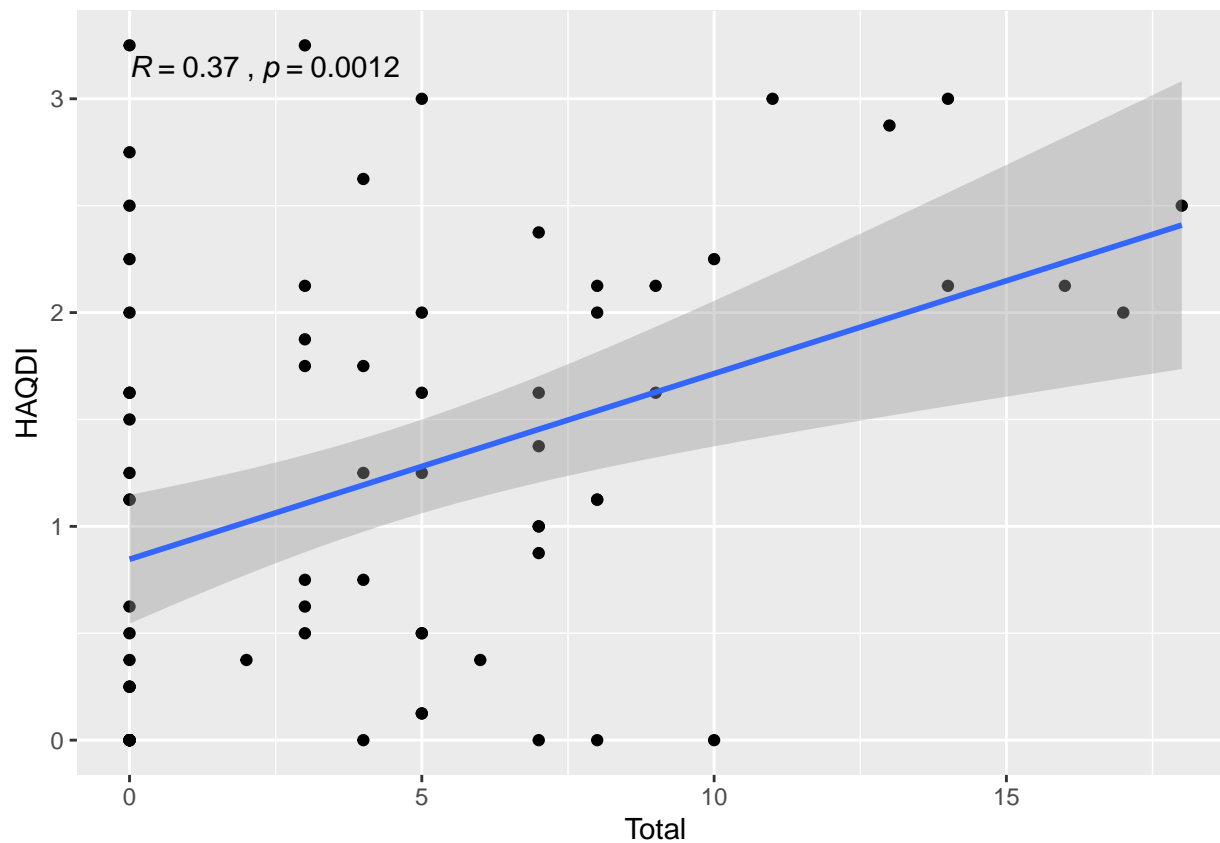
```
##TNS saistība ar HAQDI
```

```
cor(ssc$Total,ssc$HAQDI,use='pairwise.complete.obs')
```

```
## [1] 0.4033265
```

```
ssc %>% ggplot(aes(Total,HAQDI))+geom_point()+geom_smooth(method=lm)+stat_cor(method = "spearman")
```





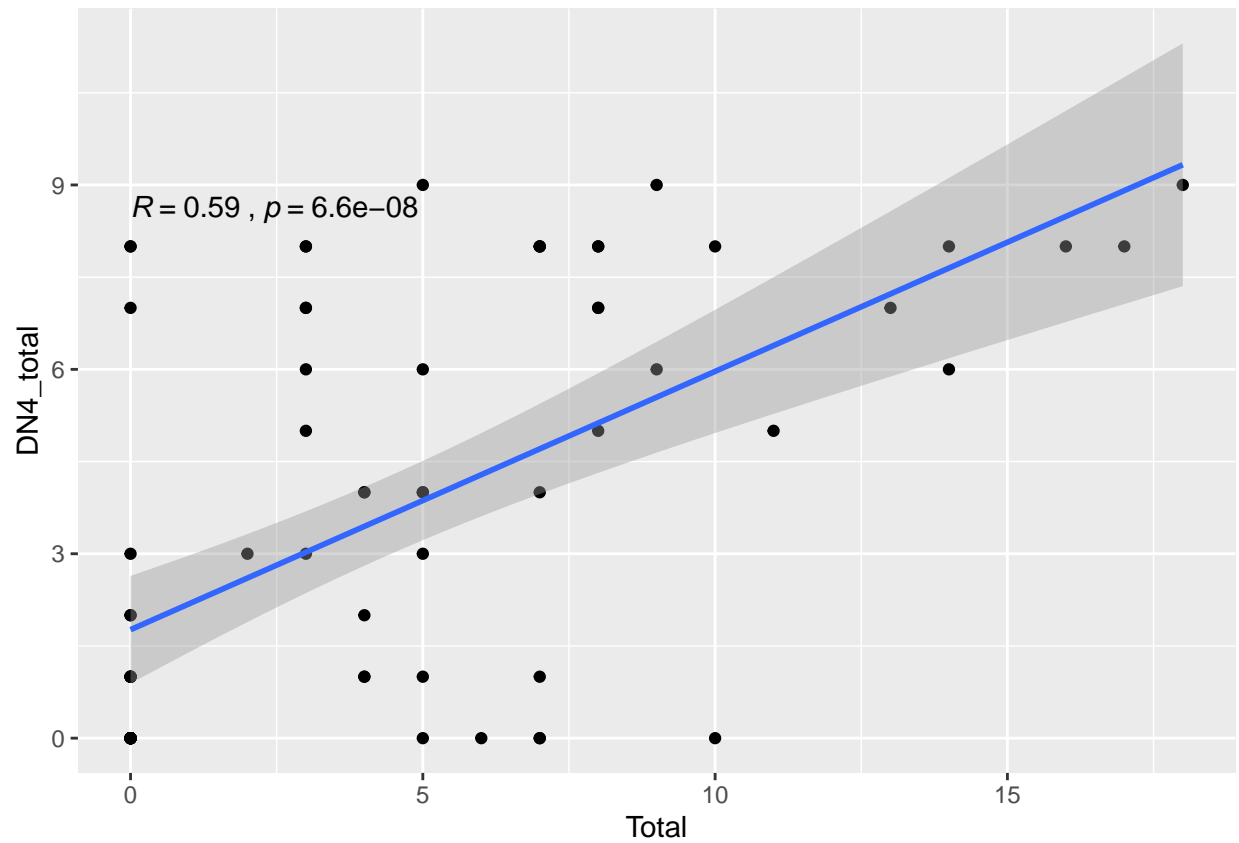
Augstāks total TNS saistīts ar lielāku HAQDI (vai tas nozīmē, ka smagāka neiropātija = labāka dzīves kvalitāte????? vai lielāks HAQDI nozīmē, ka ir sliktāk?)

##TNS saistība ar DN4

```
cor(ssc$Total,ssc$DN4_total,use='pairwise.complete.obs')
```

```
## [1] 0.5901333
```

```
ssc %>% ggplot(aes(Total,DN4_total))+geom_point()+geom_smooth(method=lm)+stat_cor(method = "spearman")
```

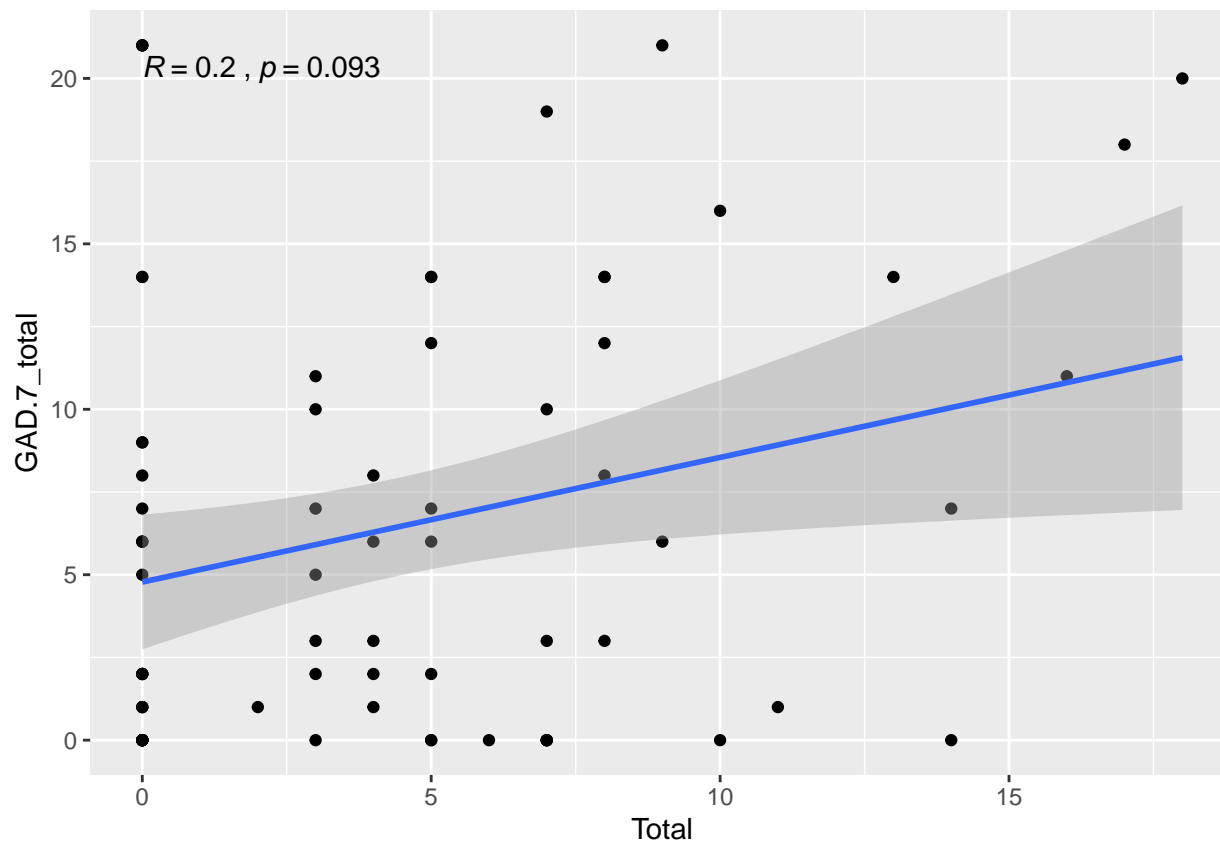


##TNS saistība ar GAD7

```
cor(ssc$Total,ssc$GAD.7_total,use='pairwise.complete.obs')
```

```
## [1] 0.2685259
```

```
ssc %>% ggplot(aes(Total,GAD.7_total))+geom_point()+geom_smooth(method=lm)+stat_cor(method = "spearman")
```



TNS ir vidēji spēcīgā saistība ar DN4 un vāja saistība ar GAD7 (makes sense, pareizi? smagāka neiropatija=augstāka neiropatiskās sāpes)

---

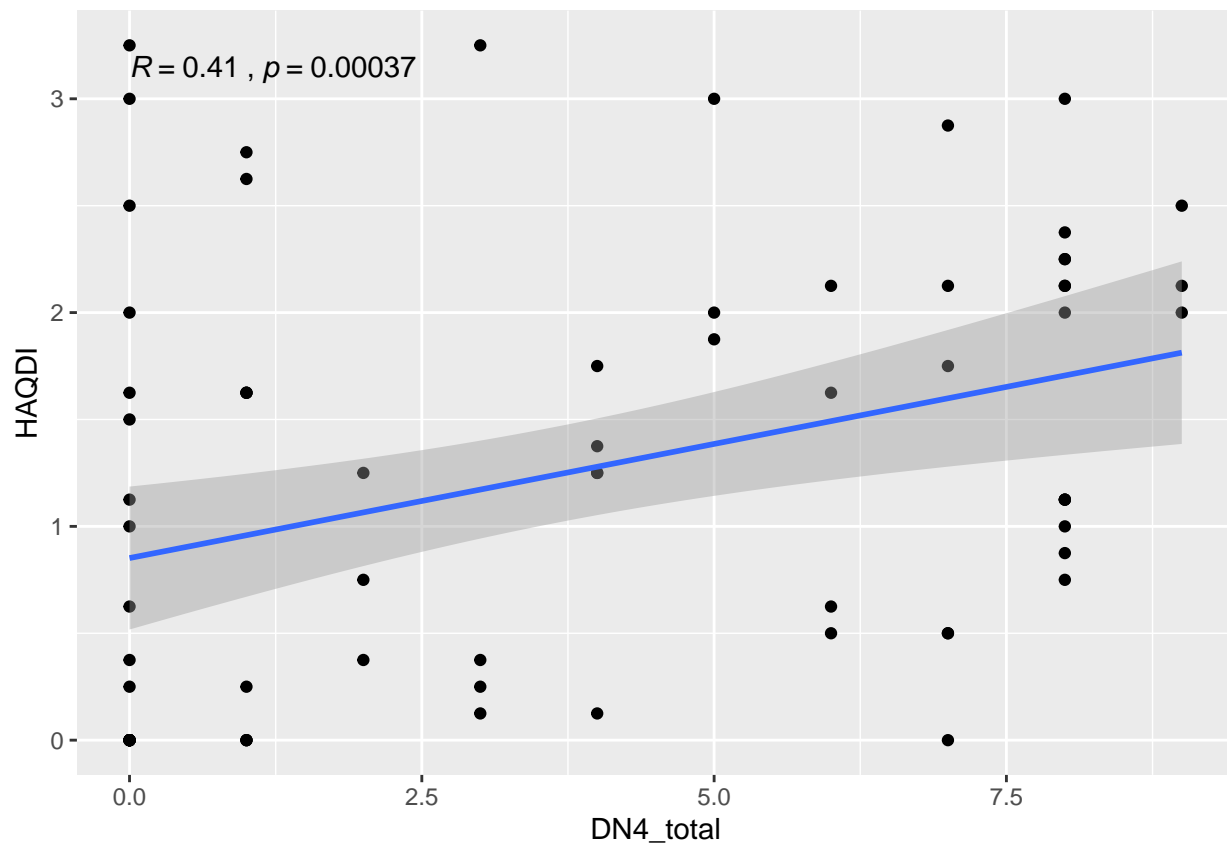
```
#Total DN4/GAD7 saistība ar HAQDI
```

```
##DN4 saistība ar HAQDI
```

```
cor(ssc$DN4_total,ssc$HAQDI,use='pairwise.complete.obs')
```

```
## [1] 0.3535831
```

```
ssc %>% ggplot(aes(DN4_total,HAQDI))+geom_point()+geom_smooth(method=lm)+stat_cor(method = "spearman")
```



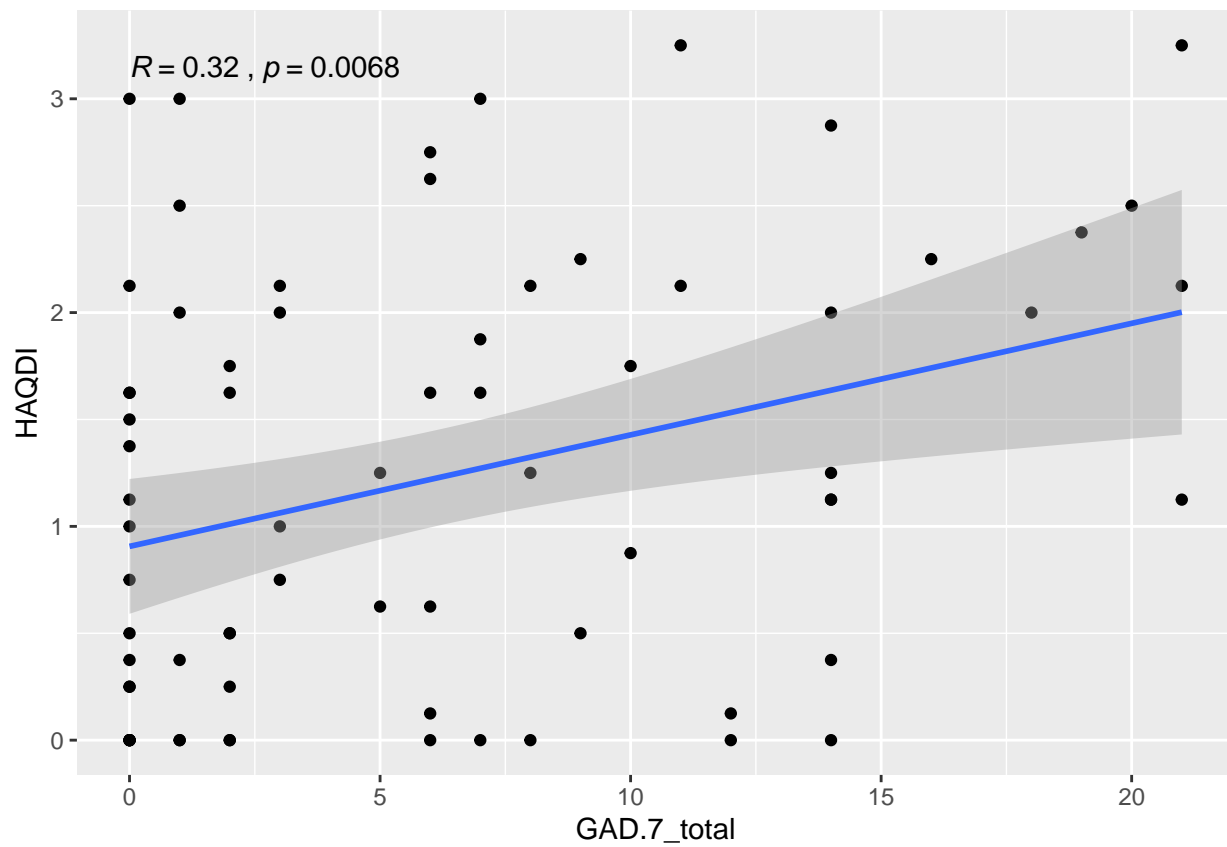
Vidēji stipra saistība starp DN4 un HAQDI

##GAD7 saistība ar HAQDI

```
cor(ssc$GAD.7_total,ssc$HAQDI,use='pairwise.complete.obs')
```

```
## [1] 0.329856
```

```
ssc %>% ggplot(aes(GAD.7_total,HAQDI))+geom_point()+geom_smooth(method=lm)+stat_cor(method = "spearman")
```



Vidēji stipra saistība starp GAD7 un HAQDI